PATENT
Attorney Docket **056159-5241-US**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

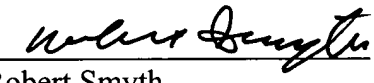
Inventors: **Steven COLLIVER *et al.***)
)
U.S. National Phase of **PCT/EP03/01465**) Art Unit: **Not Assigned**
)
International Filing Date: **February 13, 2003**) Examiner: **Not Assigned**
)
For: **NUTRITIONALLY ENHANCED PLANTS**)

Commissioner for Patents
Washington, D.C. 20231

STATEMENT ACCOMPANYING SEQUENCE LISTING

The undersigned hereby states upon information and belief that the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed and that the information recorded on the diskette submitted concurrently herewith is identical to the written Sequence Listing submitted herewith.

Respectfully submitted,
Morgan, Lewis & Bockius LLP



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SEQUENCE LISTING

<110> COLLIVER, Steven Peter
DOBB, Roy Thomas
van der HIJDEN, Hendrikus Theodorus Wilhelmus Maria

<120> PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS

<130> 56159-5241

<150> PCT/EP03/01465
<151> 2003-02-13

<150> EP 02251404.6
<151> 2002-02-28

<160> 59

<170> PatentIn version 3.2

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gaacaagctc ttggtgaggc tttgaatgag gctattcaac ttggtcttgt cactagagaa 240

cagctttttg ttacttctaa actttgggtt actgaaaatc atcctcacct tgttcttcct 300

gctctacaaa aatctctcaa gactcttcag ttggattact tggatttgta tttgattcat 360

tggccactta gttctcagcc cggaaagttt tcatttccaa ttgatgtggc tgatctattg 420

ccatttgatg taaaaggtgt gtgggaatcc atggaagagg ctttgagact tggactcacg 480

aaagctattg gtgtcagtaa cttctctgtc aagaaacttc aaaagctact atctgttgcc 540

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agagaatttt gcaatgaaaa tggaatagtg ttgactgcat tttcaccgtt gaggaaaggc 660

gccagccgag gagcaaatga ggttatggag aatgatatgc ttaaacagat tgcagatgct 720

catggaaagt ctattgcaca aatttctctg agatggttat atgaacaagg aatcactttt 780

gttccaaaga gctatgataa ggagagaatg agtcaaaatt tgagaatctt tgattggaca 840

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<213> Pisum sativum

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Cys Lys Lys Asp Thr Lys Glu Ala Ile Ile Glu Ala Ile Lys Gln Gly
        35                  40                  45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
    50                  55                  60

Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
65                  70                  75                  80

Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
                85                  90                  95

Leu Val Leu Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp
            100                 105                 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
        115                 120                 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
    130                 135                 140

Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
145                 150                 155                 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu
                165                 170                 175

Leu Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
            180                 185                 190
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Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Glu Asn Gly
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Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
210 215 220

Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
225 230 235 240

His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
245 250 255

Gly Ile Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln
260 265 270

Asn Leu Arg Ile Phe Asp Trp Thr Leu Thr Lys Glu Asp His Glu Lys
275 280 285

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Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
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atcgctcgcg aggttcttaa gatctttggc gaatacagcc tcactgactt catctggcca 660

ttgaagcatc tcaaggttgg aaagtatgag aagaggatcg acgacatctt gaacaagttc 720

gaccctgtcg ttgaaagggt catcaagaag cgccgtgaga tcgtgaggag gagaaagaac 780

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tttttctcgg caggaacaga ctcaacagcg gtggcaacag agtgggcatt ggcagaactc 960

atcaacaatc ctaaggtgtt ggaaaaggct cgtgaggagg tctacagtgt tgtgggaaag 1020

gacagacttg tggacgaagt tgacactcaa aaccttcctt acattagagc aatcgtgaag 1080

gagacattcc gcatgcaccc gccactccca gtggtcaaaa gaaagtgcac agaagagtgt 1140

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<212> PRT
<213> Glycine max

<400> 4

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Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 55 60

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Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
65                  70                  75                  80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
                85                  90                  95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
            100                 105                 110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
        115                 120                 125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
    130                 135                 140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
145                 150                 155                 160

Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
                165                 170                 175

Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
            180                 185                 190

Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
        195                 200                 205

Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
    210                 215                 220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
225                 230                 235                 240

Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
                245                 250                 255

Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
            260                 265                 270

Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
        275                 280                 285
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Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
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Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
305                 310                 315                 320

Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
                325                 330                 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
            340                 345                 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
        355                 360                 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
    370                 375                 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
385                 390                 395                 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
                405                 410                 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
            420                 425                 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
        435                 440                 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
    450                 455                 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465                 470                 475                 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
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Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
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<212> DNA
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gaggggaagt tcataaaatt cactggcata ggagtgtatt tggaagatac agcagtggat 180

tcactcgcca ccaagtggaa gggtaagagt tcacaagagc tgcaggactc ccttgacttc 240

ttcagagaca tcatttcaag tccctctgag aagttaattc gagggtccaa gctgaggcca 300

ttgagtggcg tggagtattc aagaaaggtg atggagaatt gtgtggcaca catgaagtct 360

gctggaactt atggtgaagc agaggccaca gccattgaaa aatttgcaga agccttcagg 420

aaggtggatt ttccaccagg ttcctctgtt ttctaccgac aatcaacaga tggaaaatta 480

gggcttagtt tctctttgga tgacacgata ccagaagaag aggctgtagt tatagagaac 540

aaggcactct cagaggcagt gttagagacc atgattggcg agcatgctgt ttcccctgat 600

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ggaaactgat 670

<210> 6
<211> 222
<212> PRT
<213> Lotus corniculatus

<400> 6

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Ala Ser Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly
20 25 30

Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr
35 40 45

Gly Ile Gly Val Tyr Leu Glu Asp Thr Ala Val Asp Ser Leu Ala Thr
50 55 60

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Lys Trp Lys Gly Lys Ser Ser Gln Glu Leu Gln Asp Ser Leu Asp Phe
65                  70                  75                  80

Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu Lys Leu Ile Arg Gly Ser
                85                  90                  95

Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg Lys Val Met Glu
            100                 105                 110

Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu Ala Glu
        115                 120                 125

Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
    130                 135                 140

Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu
145                 150                 155                 160

Gly Leu Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val
                165                 170                 175

Val Ile Glu Asn Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile
            180                 185                 190

Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg
        195                 200                 205

Leu Pro Ile Val Met Asn Gln Gly Leu Leu Leu Thr Gly Asn
    210                 215                 220
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<220>
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regions of various known CHR's

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<210> 8

<211> 8
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<220>
<223> Description of Artificial Sequence:conserved
regions of various known CHR's

<400> 8

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<210> 9
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<212> DNA
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<220>
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<210> 11
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<213> Artificial Sequence

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<211> 17
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<400> 22
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<210> 23
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<210> 24
<211> 30
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<210> 33
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<210> 39
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caagggtctt gttgtagac 79

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atggaagagg ctttgaga 78

<210> 52
<211> 25
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<220>
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<400> 52
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<210> 53
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<400> 53
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<210> 54
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<210> 55
<211> 42
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<223> Description of Artificial Sequence:primer

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